

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:30:12 ; Search time 16.0286 Seconds
(without alignments)
28.464 Million cell updates/sec

Title: US-09-856-070-23
Perfect score: 55
Sequence: 1 EIMLRQDYEE 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 11476328 residues

Total number of hits satisfying chosen parameters: 112892

```
Minimum DB seq length: 0
Maximum DB seq length: 20
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	55	100	0	1	E2F1_HUMAN	P151975 bos taurus
2	55	100	0	1	E2F1_HUMAN	P153111 homo sapien
3	52	94.5	555	1	E2F1_MOUSE	P26040 mus musculus
4	39	70.9	866	1	RA50_MOUSE	O33600 sulfobolus
5	36	65.5	715	1	RB52_BAPAE	Q4RSP7 brachydano
6	36	65.5	2472	1	SPCN_HUMAN	Q13813 homo sapien
7	36	65.5	2472	1	SECN_RAT	P16086 rattus norv
8	36	65.5	2477	1	SPCN_CHICK	P07751 gallus gall
9	35	63.6	852	1	AA01_HUMAN	P12814 homo sapien
10	35	63.6	892	1	AA01_RAT	Q971p2 rattus norv
11	35	63.6	964	1	PE01_MOUSE	Q9QX81 mus musculus
12	35	63.6	4473	1	PE01_CRIGR	Q9J155 cricellulus
13	35	63.6	4684	1	PE01_HUMAN	Q15149 homo sapien
14	35	63.6	4687	1	PE1_PAT	P04027 rattus norv
15	34	61.8	332	1	KC2A_MALTE	P28523 zea mays (m
16	34	61.8	333	1	KC31_ARATH	Q08467 arabidopsis
17	34	61.8	333	1	KC22_ARATH	Q08466 arabidopsis
18	34	61.8	333	1	KC23_ARATH	Q08417 arabidopsis
19	34	61.8	365	1	EC01_SCHPO	Q94116 schizosacch
20	34	61.8	367	1	YGH5_YEAST	P53159 saccharomyc
21	34	61.8	435	1	FUT4_HUMAN	P22083 homo sapien
22	34	61.8	467	1	INVO_MOUSE	P48997 mus musculu
23	34	61.8	544	1	TSO1_METTL	Q93824 methanococc
24	34	61.8	741	1	TS02_PAPMF	P11929 drosoephila
25	34	61.8	860	1	PAG6_PYPAR	P54268 pyrococcus
26	34	61.8	978	1	RA50_AQUAF	Q67124 aquifex aco
27	33	60.0	177	1	PURE_F0RAM	Q44679 verycoccate
28	33	60.0	195	1	V11A_H17	P03746 bacteriopho
29	33	60.0	245	1	YH74_YEAST	Q05024 saccharomyc
30	33	60.0	258	1	YF08_MYCTU	Q18859 mycobacteri
31	33	60.0	270	1	CFP6_SCHPO	Q9P765 schizosacch
32	33	60.0	320	1	H1P1_HUMAN	P54257 homo sapien
33	33	60.0	522	1	CPV1_ORNEN	P70091 orochromis

RESULTS

E2R1_BOVIN STANDARD; PRT; 580 AA.
 ID E2R1_BOVIN
 AC P31976;
 DT 01-JUL-1993 (Rel. 26, Created)
 DI 01-JUL-1993 (Rel. 26, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE E2R1 (p8) (Cytovillin) (Villin 2).
 GN Vill2.
 OS Bos taurus (Bovine).
 OC Eukaryota, Metazoa, Chordata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Perartiodactyla, Ruminantia, Pecora; Bovidae;
 OC Bovinae, Bovinae, Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 PA Bergson C M, Zhao H, Saijoh K, Duman P S, Nestler E J.;
 RT "Ezrin and osteonectin, two proteins associated with cell shape and
 RT growth, are enriched in the locus coeruleus";
 RL Mol. Cell. Neurosci. 4:64-73(1993).
 [2]
 RN SEQUENCE OF 1-15 AND 126-140.
 RP
 RC TISSUE=Kidney;
 RC Madsen=96235137; Pubmed=8660651;
 kX Cabot A, Gerbasi M C, Bouet F, Riviere S.;
 RA "Proteins and their amino acid compositions: uniqueness, variability,
 RT and applications";
 RT Arch. Biochem. Biophys. 330:229-237(1996).
 CC -1- FUNCTION: PROBABLY INVOLVED IN CHANNELS OF MAJ-P CYTOSKELETAL
 CC STRUCTURES TO THE PLASMA MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: MICROVILLI; PERIPHEAL MEMBRANE PROTEIN
 CC (CYTOPLASMIC SIDE).
 CC -1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
 CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
 CC
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 CC
 DR EMBL: M98498; AAA30510.1;
 DR InterPro: IPR000299; Band 4.1.
 TR UniProtKB: IPR000798; I2/rad/ems2in.
 DR Pfam: PF00373; Band 4.1;
 DR Pfam: PF00769; ERM; 1.
 DR PRINTS: PS00935; HAND01.
 DR SMART: SM00295; H41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS06664; BAND_41_2; 1.
 DR PROSITE: PS50057; BAND_41_3; 1.
 KW Structural Protein, Cytoskeleton, Phosphorylation.
 FT INIT MET 0

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FT DOMAIN 57 224 BAND 4.1-LIKE.
FT MOD_RES 145 145 PHOSPHORYLATION (BY PDGFR)
PI MOD_RES 353 353 (BY SIMILARITY).
PI MOD_RES 353 353 PHOSPHORYLATION (BY PDGFR)
PI MOD_RES 353 353 PHOSPHORYLATION (BY PDGFR)
SQ SEQUENCE 580 AA: 68629 MW: 62665.450200000000 CRC64:
Query Match 100.0%; Score 55; DB 1; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 11, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 ELMRLQDYEE 11
DB 345 ELMRLQDYEE 355
RESULT 2
EZRL_HUMAN STANDARD: PRT: 585 AA
AC P15311; P24714; Q9NSJ4;
DE 01-APR-1990 (Ref. 14, Created)
DE 01-NOV-1991 (Ref. 20, Last sequence update)
DE 15-JUN-2002 (Ref. 41, Last annotation update)
DE Ecrin (p81) (Cytoovillin) (Willin 2).
GN VIL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_TaxID=9606;
IN 11
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE-90076135; PubMed-2591371;
RA Gould K.L., Bretschel A., Esch F.S., Hunter T.;
PI "cDNA cloning and sequencing of the protein tyrosine kinase
substrate, crin, reveals homology to band 4.1.";
RL EMBO J. 8:4133-4142(1989).
IN 12
RP SEQUENCE FROM N.A.
RC TISSUE-placenta;
RX MEDLINE-89380299; PubMed-2674140;
RA Turunen O., Winkvist R., Pakkanen R., Grzeschik R.H., Wahlstrom T.,
Vaheti A.;
PI "Cytoovillin, a microvillar Mr 75,000 protein, cDNA sequence,
prokaryotic expression, and chromosomal localization.";
RL J. Biol. Chem. 264:16727-16732(1989).
IN 13
RP SEQUENCE FROM N.A.
RA Odenwälder B., Obermaier B., Mewes H.-W., Weil B., Wiemann S.;
PI Submitted (MAR 2000) to the EMBL/Genbank/DBJ databases.
IN 14
RP SEQUENCE OF 171-179 AND 342-349.
RX MEDLINE-96411348; PubMed-8713105;
RA Parton M., Moritz R.L., Braker H., Kelso A., Simpson R.J.;
PI "Identification of the 70kD heat shock cognate protein (Hsc70) and
alpha-actinin 1 as novel phosphotyrosine-containing proteins in T
lymphocytes.";
RL Biochem. Biophys. Res. Commun. 224:666-674(1996).
IN 15
RP PHOSPHORYLATION BY PDGFR
RX MEDLINE-92406868; PubMed-1382070;
RA Kriegl J., Hunter T.;
PI "Identification of the two major epidermal growth factor-induced
tyrosine phosphorylation sites in the microvillar core protein
crin.";
RL J. Biol. Chem. 267:19258-19265(1992).
IN 16
RP PHOSPHORYLATION.
RX MEDLINE-92486649; PubMed-1381489;
RA Parton M., Burgess W.H., Chen D., Braker H.J., Bretscher A.,
Smolnik L.F.;
PI "Identification of crin as an 81 kDa tyrosine-phosphorylated protein
in T cells.";
RL J. Immunol. 149:1847-1852(1992).
CC -1 FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
STRUCTURES TO THE PLASMA MEMBRANE.
CC -1 SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
(CYTOPLASMIC SIDE).
CC -1 TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
EPITHELIAL CELLS.
CC -1 PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
CC -1 SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
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CC
EMBL: X51521; CAA35893.1;
EMBL: J05021; AAA61278.1; ALT_INIT.
EMBL: AL162086; CAB82418.1; ALT_INIT.
PIR: S09263; S09263.
PIR: A34400; A34400.
SWISS-2DPAGE: P15311; HUMAN.
Genew. HCR:12691. VIL2.
MIM: 123900;
InterPro: IPR000299; Band_4.1.
InterPro: IPR000794; P2/1ad/moesin.
PIR: PF00373; Band_4.1; 1.
PIR: PF00769; ERM; 1.
PRINTS: PR00935; BAND4.1.
SMART: SM00295; B41; 1.
DR PROSITE; PS00660; BAND_41_1; 1.
DR PROSITE; PS00661; BAND_41_2; 1.
DR PROSITE; PS00661; BAND_41_3; 1.
DR PROSITE; PS00661; BAND_41_4; 1.
KW Structural protein, Cytoskeleton, Phosphorylation.
FT INIT_MET 0
FT DOMAIN 57 224 BAND 4.1-LIKE.
FT MOD_RES 145 145 PHOSPHORYLATION (BY PDGFR).
FT MOD_RES 353 353 PHOSPHORYLATION (BY PDGFR).
FT CONFLICT 531 531 V -> L (IN REF. 3).
SQ SEQUENCE 585 AA: 69267 MW: 24844.014063806000 CRC64:
Query Match 100.0%; Score 55; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 11, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 ELMRLQDYEE 11
DB 345 ELMRLQDYEE 355
RESULT 3
EZRL_MOUSE STANDARD: PRT: 585 AA.
AC P26040;
DE 01-MAY-1992 (Ref. 22, Created)
DE 01-MAY-1992 (Ref. 22, Last sequence update)
DE 16-OCT-2001 (Ref. 40, Last annotation update)
DE Ecrin (p81) (Cytoovillin) (Willin 2).
GN VIL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurostomata; Muridae; Mus.
CX NCBI_TaxID=10090;
IN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-92064615; PubMed-1955455;
RA Funayama N., Naqaiuchi A., Sato N., Tsukita S., Tsukita S.;
PI "Radixin is a novel member of the band 4.1 family.";
RL J. Cell Biol. 115:1039-1048(1991).
CC -1 FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
STRUCTURES TO THE PLASMA MEMBRANE.
CC -1 SUBCELLULAR LOCATION: Cytoplasmic.

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CC -1- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
 CC EPITHELIAL CELLS.
 CC -1- PIM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES
 CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
 CC
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DR EMBL: X60671; CAA43086.1; -
 DR PIR: B41129; B41129.
 DR MGD: M01:98931; Vili2.
 DR InterPro: IPR000294; band_4.1.
 DR InterPro: IPR000798; k2/rad/moesin.
 DR Pfam: PF00373; Band_41; 1.
 DR Pfam: PF00769; ERM; 1.
 DR PRINTS: PF00935; BAND41.
 DR SMART: SM00295; B41; 1.
 DR PROSITE: PS00660; BAND_41_1; 1.
 DR PROSITE: PS00661; BAND_41_2; 1.
 DR PROSITE: PS00662; BAND_41_3; 1.
 DR Structural protein; Cytoskeleton; phosphorylation.
 KW INIT_MET 0 BY SIMILARITY.
 FT DOMAIN 57 224 BAND 4.1-LIKE.
 FT MOD_RES 145 145 PHOSPHORYLATION (BY PDEFR)
 FT MOD_RES 353 353 (BY SIMILARITY).
 FT MOD_RES 353 353 PHOSPHORYLATION (BY PDEFR)
 FT PHOSPHORYLATION (BY PDEFR)
 FT PHOSPHORYLATION (BY PDEFR)
 SQ SEQUENCE 585 AA: 69214 MW: 20574222.200502 CRC64;

Query Match 94.5%, Score 52; DB 1; Length 585;
 Best Local Similarity 90.4%; Pred. No. 0 019;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
 |||||
 DB 345 ELMRLQDYEQ 355

RESULT 4
 ID PASO_SILAC STANDARD; PRT: 886 AA.
 AC Q33600;
 DI 16-OCT-2001 (Rel. 40; Created)
 DI 16-OCT-2001 (Rel. 40; Last sequence update)
 DI 16-OCT-2001 (Rel. 40; Last annotation update)
 DE DNA double-strand break repair rad50 ATPase.
 GN PABPn
 OS Sulfolobus acidocaldarius.
 CC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 CC Sulfolobus.
 CC NCBI_TaxID=2285;
 CC [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN A107-45-107; M-FP: 1175; DSM 850;
 RX MEDLINE: 97362314; PubMed-9211741;
 RT Elie C., Haucher M.P., Fondrat C., Forterre P.,
 FT "A protein related to eucarya, and bacterial DNA motor proteins in the
 FT hyperthermophilic archaeon Sulfolobus acidocaldarius".
 RL J. Mol. Evol. 45:107-114(1997).
 CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
 CC rad50/mrell complex possesses single strand endonuclease activity
 CC and ATP dependent double strand specific exonuclease activity.
 CC Rad50 provides an ATP-dependent control of mrell by unwinding
 CC and/or repositioning DNA ends into the mrell active site (By
 CC similarity).
 CC -1- SUBUNIT: Forms a complex with mrell (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.

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DR EMBL: Y10687; CAA71688.1; -
 DR InterPro: IPR003439; ABC_Transport; 1.
 DR InterPro: IPR003395; SMC_N.
 DR Pfam: PF02463; SMC_N; 1.
 DR Pfam: PD000006; ABC_Transport; 1.
 DR KW DNA repair; Hydrolase; ATP-binding; Coiled coil.
 FT NP_BIND 30 37 ATP (BY SIMILARITY).
 FT DOMAIN 174 727 COILED COIL (POTENTIAL).
 SQ SEQUENCE 886 AA: 10557 MW: 100046149.14104 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 886;
 Best Local Similarity 63.6%; Pred. No. 10;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYEE 11
 |||||
 DB 259 FTAIRKDFP 269

RESULT 5

RRS2_VRAPE STANDARD; PRT: 715 AA.
 AC Q98SP7;
 DI 15-JUN-2002 (Rel. 41; Created)
 DI 15-JUN-2002 (Rel. 41; Last sequence update)
 DI 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Bardet-Biedl syndrome 2 protein homolog.
 GN BBS2.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 CC NCBI_TaxID=7955;
 CC [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 21181710; PubMed-11285252;
 RA Nishimura D.Y., Searby C.C., Carmi P., Elbedour K., Van Maldergem L.,
 RA Fildes A.B., Lam P.L., Powell R.P., Swiderski P.E., Budge K.E.,
 RA Haider N.B., Switek-Black A.E., Ying L., Duhl D.M., Gorman S.M.,
 RA Heon E., Tannock A., Bonneau D., Biesecker L.G., Jacobson S.G.,
 RA Stone E.M., Sheffield V.C.;
 FT "Positional cloning of a novel gene on chromosome 16q causing
 FT Bardet-Biedl syndrome (BBS2)".
 RL Hum. Mol. Genet. 10:865-874(2001).

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DR EMBL: AF342739; AAC28555.1; -
 SQ SEQUENCE 715 AA: 70125 MW: 1267700.4530756 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 715;
 Best Local Similarity 70.0%; Pred. No. 30;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMLPLQDYEE 11
 |||||
 DB 348 LMLELRNYEE 357

RESULT 6

SPCN_HUMAN STANDARD: PRT: 2472 AA.

AC Q13814; G16606; Q9P0V0; Q14186;

DE 01-NOV-1997 (Ref. 35, Created)

DE 01-NOV-1997 (Ref. 35, Last sequence update)

DE 15-JUN-2002 (Ref. 41, Last annotation update)

DE Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)

DE (Alpha-II spectrin) (Pofrin alpha chain).

GN SPTAN1 OR SPTA2

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

EN [1]

KX MEDLINE=90170948; PubMed=2307671;

KA Moon R.T., McMahon A.P.;

KA "Generation of diversity in nonerythroid spectrins. Multiple polypeptides are predicted by sequence analysis of cDNAs encompassing the coding region of human nonerythroid alpha-spectrin.",

KL J. Biol. Chem. 265:4427-4434(1990).

EN [2]

EP SEQUENCE FROM N.A.

EC Tissue-Fetal brain;

KA Daniel C.D., Morrow J.S.;

KA "Complete cDNA sequence of human alpha II fetal brain spectrin.";

KL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.

EN [3]

EP SEQUENCE OF 676-1595 FROM N.A.

EC TISSUE-Lung;

KA MEDLINE=88083942; PubMed=3691949;

KA McMahon A.P., Moon R.T.;

KA "Structure and evolution of a non-erythroid spectrin, human alpha-fodrin.",

KL Biochem. Soc. Trans. 15:804-807(1987).

EN [4]

EP SEQUENCE OF 676-1595 FROM N.A.

KA MEDLINE=87277023; PubMed=3038643;

KA McMahon A.P., Gleichhaus D.H., Champion J.E., Railes J.A., Jacey S., Carritt B., Hencham S.K., Moon R.T.;

KA "cDNA cloning, sequencing and chromosome mapping of a non-erythroid spectrin, human alpha-fodrin.",

KL Differentiation 34:68-78(1987).

EN [5]

EP FRATUM.

KA McMahon A.P., Gleichhaus D.H., Champion J.E., Railes J.A., Jacey S., Carritt B., Hencham S.K., Moon R.T.;

KL Differentiation 34:241-241(1987).

EN [6]

EP SEQUENCE OF 811-1529 FROM N.A., VARIANT ILE-1300, AND MUTAGENESIS.

EC TISSUE-Fetal brain;

KA MEDLINE=97146462; PubMed=8993318;

KA Stabach P.R., Glancz C.D., Glantz S.B., Zhang Z., Morrow J.S.;

KA "Site-directed mutagenesis of alpha II spectrin at codon 1175 modulates its macropain susceptibility.",

KL Biochemistry 36:57-65(1997).

EN [7]

EP SEQUENCE OF 1073-1349 FROM N.A.

KA Murakami N., Speed W.C., Seaman M.I., Zychowski P.L., Welterberg L., Pakstis A.L., Kidd J.P., Kidd K.K.;

KA "Association and linkage analyses of the nonerythroid alpha-spectrin (SPTAN1) gene on chromosome 9q34 with a large Swedish kindred.",

KL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases

CC -1- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION, INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS THIS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE CYTOSKELETON AT THE MEMBRANE

CC -1- SUBUNIT: LIKE FODRIN-LIKE PROTEINS, THE SPECTRIN-LIKE PROTEINS ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO TETRAMERS.

CC -1- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

CC -1- SIMILARITY: CONTAINS 23 SPECTRIN REPEATS.

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EMBL: J05243; AAA51790.1; -

EMBL: U83867; AAB41498.1; -

EMBL: M24773; AAS52468.1; -

EMBL: M18627; AAA51702.1; -

EMBL: U26396; AAB0364.1; -

EMBL: AF148608; AAF25672.1; -

HSSP: P07751; IAEY.

Gene: HGNC:11273; SPTAN1.

MIM: 182810; -

InterPro: IPR002048; EF-hand.

InterPro: IPR001452; SH3.

InterPro: IPR002017; Spectrin.

Pfam: PF00018; SH3; 1.

Pfam: PF00036; ethand; 4.

Pfam: PF00435; spectrin; 32.

PRINTS: PR00452; SH3DOMAIN.

ProDom: PD000012; EF-hand; 1.

ProDom: PD000066; SH3; 1.

SMART: SM00054; EFh; 2.

SMART: SM00326; SH3; 1.

SMART: SM00150; SPC; 20.

PROSITE: PS00018; EF-HAND; 1.

PROSITE: PS50002; SH3; 1.

KW Cytoskeleton, Membrane, Calmodulin binding, Actin-binding, Capping protein, Calcium-binding, Repeat, SH3 domain, Polymorphism.

FT REPEAT 10 42

FT SPECTRIN 1.

FT REPEAT 44 147

FT SPECTRIN 2.

FT REPEAT 149 253

FT SPECTRIN 3.

FT REPEAT 255 359

FT SPECTRIN 4.

FT REPEAT 361 465

FT SPECTRIN 5.

FT REPEAT 467 571

FT SPECTRIN 6.

FT REPEAT 573 676

FT SPECTRIN 7.

FT REPEAT 678 782

FT SPECTRIN 8.

FT REPEAT 784 888

FT SPECTRIN 9.

FT REPEAT 890 955

FT SPECTRIN 10.

FT SH3.

FT REPEAT 967 1026

FT SPECTRIN 11.

FT REPEAT 1062 1089

FT SPECTRIN 12.

FT REPEAT 1091 1161

FT SPECTRIN 13.

FT REPEAT 1208 1231

FT SPECTRIN 14.

FT REPEAT 1233 1337

FT SPECTRIN 15.

FT REPEAT 1339 1443

FT SPECTRIN 16.

FT REPEAT 1445 1549

FT SPECTRIN 17.

FT REPEAT 1551 1656

FT SPECTRIN 18.

FT REPEAT 1658 1762

FT SPECTRIN 19.

FT REPEAT 1764 1868

FT SPECTRIN 20.

FT REPEAT 1870 1974

FT SPECTRIN 21.

FT REPEAT 1976 2081

FT SPECTRIN 22.

FT REPEAT 2091 2195

FT SPECTRIN 23.

FT REPEAT 2205 2310

FT EF-HAND 1 (POTENTIAL).

FT CA_BIND 2336 2347

FT EF-HAND 2 (POTENTIAL).

FT CA_BIND 2379 2390

FT SITE 1176 1177

FT VAPANT 1300 1300

FT /FTID-VAR_012327.

FT N -> K (IN REF. 2).

FT F -> S (IN REF. 2).

FT V -> I (IN REF. 2).

FT Q -> Q/SK/L (IN REF. 2).

FT F -> R (IN REF. 3 AND 4).

FT N -> S (IN REF. 2).

FT IA -> FD (IN REF. 2).

FT A -> D (IN REF. 2).

FT CONFLICT 2347 2348 DG 3 EF (IN REF. 2).
 FT CONFLICT 2448 2448 I 3 Y (IN REF. 3).
 SQ SEQUENCE 2472 AA; 284279 MW; CQA19F4452A70280 GRC64.

Query Match 65.5% Score 36; DB 1; Length 2472;
 Best Local Similarity 63.6%; From No. 1 to 40;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0.

OY 1 ELMRLQYQE 11
 ||| | |||
 DB 970 ELVIALYDQE 980

RESULT 7
 SPQN_RAT STANDARD; PRT: 2472 AA.
 AC P16086; P70477; O88653;
 DI 01-APR-1990 (Rel. 14, Created)
 DI 15-JUN-2002 (Rel. 41, Last sequence update)
 DI 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
 DE (Alpha-II spectrin) (Fodrin alpha chain).
 GN SPAN1 OR SP1A2.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Misc; TISSUE-Liver;
 PA Kalamazaki P.; Garzanti P.;
 RT "Structural and functional characterization of the calmodulin and
 RT calpain binding domains of rat liver alphaII spectrin."
 RL Submitted (Aug-1998) to the EMBL/GenBank/ODJ databases.
 FN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RA Zhou D.; Ursell L.A.; Porter N.C.; Pandall W.P.; Bloch P.T.;
 RT "Expression cloning of alpha-fodrin from rat skeletal muscle."
 RL Submitted (Aug-1998) to the EMBL/GenBank/ODJ databases.
 FN [3]
 RP SEQUENCE OF 1292 2321 FROM N.A.
 RC TISSUE-Kidney;
 EX MEDLINE=8937227; F.B.M.-8753883.
 RA Hong W.; Doyle B.;
 RT "Cloning and analysis of cDNA clones for rat kidney alpha-spectrin."
 FI J Biol Chem 264:12758-12764 (1989)
 CC -!- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SEPTATION.
 CC INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
 CC THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
 CC CYTOSKELETON AT THE MEMBRANE (BY SIMILARITY).
 CC -!- SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
 CC ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
 CC TETRAMERS.
 CC -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 SPECTRIN REPEATS

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 CC or send an email to license@sib-sib.ch).
 CC -----
 DB EMBL: X90845; CAA62350.1; -;
 DB EMBL: AF084186; AAC33127.1; -;
 DB EMBL: J04828; AAA0770.1; -;
 DB DIB: A32612; A32612.
 DB HSP: P07751; IAT3.
 DB InterPro: IPR002048; EF-hand

DR InterPro: IPR001452; SH3.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00018; SH3_1.
 DR Pfam: PF00036; efhand; 2.
 DR Pfam: PF00435; spectrin; 33.
 DR SMART: SM00014; EFL; 2.
 DR SMART: SM00156; SH3; 1.
 DR SMART: SM00150; SPEG; 29.
 DR PROSITE: PS00018; EF_HAND; 2.
 DR PROSITE: PS00002; SH3; 1.
 KW Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;
 KW Capping protein; Calcium-binding; Repeat; SH3 domain.
 FT REPEAT 10 42
 FT SPECTRIN 1.
 FT REPEAT 44 147
 FT SPECTRIN 2.
 FT REPEAT 149 253
 FT SPECTRIN 3.
 FT REPEAT 255 359
 FT SPECTRIN 4.
 FT REPEAT 361 465
 FT SPECTRIN 5.
 FT REPEAT 467 571
 FT SPECTRIN 6.
 FT REPEAT 573 676
 FT SPECTRIN 7.
 FT REPEAT 678 782
 FT SPECTRIN 8.
 FT REPEAT 784 888
 FT SPECTRIN 9.
 FT REPEAT 890 955
 FT SPECTRIN 10.
 FT DOMAIN 967 1026
 SH3.
 FT REPEAT 1062 1089
 FT SPECTRIN 11.
 FT REPEAT 1091 1161
 FT SPECTRIN 12.
 FT REPEAT 1208 1231
 FT SPECTRIN 13.
 FT REPEAT 1233 1337
 FT SPECTRIN 14.
 FT REPEAT 1339 1443
 FT SPECTRIN 15.
 FT REPEAT 1445 1549
 FT SPECTRIN 16.
 FT REPEAT 1551 1656
 FT SPECTRIN 17.
 FT REPEAT 1659 1762
 FT SPECTRIN 18.
 FT REPEAT 1764 1868
 FT SPECTRIN 19.
 FT REPEAT 1870 1974
 FT SPECTRIN 20.
 FT REPEAT 1975 2081
 FT SPECTRIN 21.
 FT REPEAT 2091 2195
 FT SPECTRIN 22.
 FT REPEAT 2205 2310
 FT SPECTRIN 23.
 FT CALBIND 2336 2347
 FT CALBIND 2349 2390
 FT CONFLICT 1329 1329
 FT CONFLICT 1514 1514
 FT CONFLICT 1702 1702
 FT CONFLICT 1971 1972
 FT CONFLICT 2205 2205
 FT CONFLICT 2310 2321
 SQ SEQUENCE 2472 AA; 284635 MW; UDDDFGIA2871278A CRC64;

Query Match 65.5% Score 36; DB 1; Length 2472;
 Best Local Similarity 63.6%; From No. 1 to 40;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0.

OY 1 ELMRLQYQE 11
 ||| | |||
 DB 970 ELVIALYDQE 980

RESULT 8
 SPQN_CHICK STANDARD; PRT: 2477 AA.
 AC P07751;
 DI 01-APR-1988 (Rel. 08, Created)
 DI 01-AUG-1991 (Rel. 19, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
 DE (Fodrin alpha chain).
 GN SPAN1 OR SP1A2.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neornithae; Galliformes; Phasianidae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE 8909238; PubMed 2610879;

KA Waseilus V. M., Saraste M., Salven P., Eraama M., Holm M.,
 KA Lehto V. P.;
 KA "Primary structure of the brain alpha-spectrin.";
 KA J. Cell Biol. 108:79-93(1989).
 RN [2]
 RP REVISIONS.
 KA Lehto V. P.;
 KA Waseilus V. M., Saraste M., Salven P., Eraama M., Holm M.,
 KA J. Cell Biol. 108:1177-1178(1989).
 RN [4]
 RP SEQUENCE OF 1695-2153 FROM N.A.
 RX MEDLINE=95284948; PubMed 4059118;
 KA Waseilus V. M., Saraste M., Knowles J., Virtanen I., Lehto V. P.;
 KA "Sequencing of the chicken non erythroid spectrin cDNA reveals an
 KA internal repetitive structure homologous to the human erythrocyte
 KA spectrin.";
 KA SPECTRIN.
 KA EMBO J. 4:1425-1440(1985).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 965-1025
 RX MEDLINE=94063299; PubMed-1279444;
 KA Musacchio A., Noble M., Pauptit R., Wieringa R., Saraste M.;
 KA "Crystal structure of a Spectrin homology 3 (SH3) domain.";
 KA Nature 359:851-855(1992).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 969-1025.
 RX MEDLINE=98363217; PubMed-9699647;
 KA Martinez J.C., Pisabarro M.F., Serrano L.;
 KA "obligatory steps in protein folding and the conformational diversity
 KA of the transition state";
 KA Nat. Struct. Biol. 5:721-729(1998)
 RN [6]
 RP STRUCTURE BY NMR OF 1763-1872.
 RX MEDLINE=98022917; PubMed-9456261;
 KA Pascual J., Puhli M., Walther D., Saraste M., Nilges M.;
 KA "Solution structure of the spectrin repeat: a left-handed
 KA antiparallel triple-helical coiled-coil.";
 KA J. Mol. Biol. 273:740-751(1997).
 RN [7]
 RP STRUCTURE BY NMR OF 2320-2403.
 RX MEDLINE=96067121; PubMed-7588621;
 KA Trave G., Lacombe J.-P., Puhli M., Saraste M., Pastore A.;
 KA "Molecular mechanism of the calcium-induced conformational change in
 KA the spectrin EF-hands.";
 KA EMBO J. 14:4922-4931(1995).
 CC [-] FUNCTION: MORPHOLOGICALLY, SPECTRIN-LIKE PROTEINS APPEAR TO BE
 CC RELATED TO SPECTRIN, SHOWING A FLEXIBLE ROD-LIKE STRUCTURE.
 CC THEY CAN BIND ACTIN BUT SEEM TO DIFFER IN THEIR CALMODULIN-
 CC BINDING ACTIVITY. IN NONERYTHROID TISSUES, SPECTRINS, IN
 CC ASSOCIATION WITH SOME OTHER PROTEINS, MAY PLAY AN IMPORTANT
 CC ROLE IN MEMBRANE ORGANIZATION
 CC [-] SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
 CC ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
 CC TETRAMERS.
 CC [-] DOMAIN: SPECTRIN-LIKE PROTEINS HAVE FIVE DOMAINS.
 CC (1) N-TERMINAL DOMAIN (N).
 CC (2) DOMAIN BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM).
 CC (3) MIDDLE DOMAIN (M).
 CC (4) DOMAIN BETWEEN THE MIDDLE AND C-TERMINAL DOMAIN (MC).
 CC (5) C-TERMINAL DOMAIN (C).
 CC NM AND MC DOMAINS ARE COMPOSED OF TYPICAL SPECTRIN 106 RESIDUES
 CC REPEATS (1-8 FOR NM AND 12-19 FOR MC) AND ARE HOMOLOGOUS TO EACH
 CC OTHER. N, M, AND C DOMAINS ARE COMPOSED OF SEQUENCES THAT DO NOT
 CC FORM TYPICAL SPECTRIN REPEATS.
 CC [-] SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
 CC [-] SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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 or send an email to license@isb-sib.ch).

CC
 DR EMBL: X14518; CAA32662.1;
 DR EMBL: X14519; CAA32663.1; ALT_SEQ.
 DR EMBL: X02593; CAA51571.1; ALT_SEQ.
 DR PIR: A30122; SJCHA.
 DR PDB: 1SHG; 31-OCT-93.
 DR PDB: 1AEY; 15-MAY-97.
 DR PDB: 1AJ3; 07-JUL-97.
 DR PDB: 1TUC; 01-AUG-96.
 DR PDB: 1TUD; 01-AUG-96.
 DR PDB: 1HK2; 16-FEB-99.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF000318; SH3; 1.
 DR Pfam: PF000316; ehand; 2.
 DR tFam: tF00435; spectrin; 23.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD000012; EF-hand; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00054; EFh; 2.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00150; SPEC; 20.
 DR PROSITE: PS00018; EF_HAND; 2.
 DR PROSITE: PS00002; SH3; 1.
 DR KQ Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;
 KW Capping protein; Calcium-binding; Repeat; SH3 domain; 3D-structure.
 FT DOMAIN 1 14
 FT REPEAT 15 119
 FT REPEAT 120 225
 FT REPEAT 226 331
 FT REPEAT 332 437
 FT REPEAT 438 543
 FT REPEAT 544 648
 FT REPEAT 649 754
 FT REPEAT 755 860
 FT REPEAT 861 966
 FT DOMAIN 967 1061
 FT DOMAIN 1062 1226
 FT DOMAIN 1227 1310
 FT DOMAIN 1311 1415
 FT DOMAIN 1416 1521
 FT DOMAIN 1522 1633
 FT DOMAIN 1634 1739
 FT DOMAIN 1740 1845
 FT DOMAIN 1846 1951
 FT DOMAIN 1952 2058
 FT DOMAIN 2059 2171
 FT DOMAIN 2172 2256
 FT CA_BIND 2343 2352
 FT CA_BIND 2384 2395
 FT STRAND 971 974
 FT STRAND 978 978
 FT TURN 983 984
 FT STRAND 985 985
 FT STRAND 988 988
 FT TURN 990 991
 FT STRAND 993 998
 FT STRAND 1004 1009
 FT TURN 1010 1011
 FT STRAND 1012 1017
 FT HELIX 1018 1020
 FT STRAND 1021 1024
 SQ SEQUENCE 2477 AA; 285361 MW; AD4C87694F6AB49 CR664;
 Query Match 65.58; Score 46; DB 1; Length 2477;
 Best local Similarity 63.58; Pred. Re. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELMRLQDVEE 11

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EMBL: AF115386; AAD12064.1;
RSPS: Q01082; IRRK.
InterPro: IPR001589; Actbind_actnin.
InterPro: IPR001715; Calponin-like.
InterPro: IPR002048; EF hand.
InterPro: IPR002017; Spectrin
Pfam: PF00036; cfband; 2.
Pfam: PF00437; CH; 2.
Pfam: PF00445; spectrin; 4.
ProDom: PM000012; EF hand; 1.
SMART: SM00034; CH; 2.
SMART: SM00054; EFH; 2.
SMART: SM00150; SPEC; 2.
PROSITE: PS00019; ACTININ_1; 1.
PROSITE: PS00020; ACTININ_2; 1.
PROSITE: PS00021; CH; 2.
PROSITE: PS00018; EF_HAND; 1.
KW Actin-binding; Calcium-binding; Repeat; Multigene family.
FI DOMAIN 1 247
ACTIN BINDING.
CH 1.
FI DOMAIN 31 145
CH 1.
FI DOMAIN 144 247
CH 2.
FI REPEAT 274 484
SPECTIN 1.
FI REPEAT 394 496
SPECTIN 2.
FI REPEAT 509 620
SPECTIN 3.
FI REPEAT 630 733
SPECTIN 4.
FI CA_BIND 759 770
EF-HAND 1 (POTENTIAL).
FI CA_BIND 800 811
EF-HAND 2 (POTENTIAL).
SQ SEQUENCE 892 AA; 10295 MW; 2360D496DCA84095 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 892;
Best local Similarity 70.0%; Prod No. 60;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELMRLQDYE 10
1 111 111
10 414 KAMLRQKQDYE 423

RESULT 11
PLEI_MOUSE STANDARD: PRT: 964 AA
AC Q9QX81: Q9QX84: Q9QX86: Q9QX87: Q9QX88: Q9QX89: Q9QX90: Q9QX91: Q9QX92: Q9QX93:
AC Q9QX94: Q9QX95: Q9QX96: Q9QX97: Q9QX98: Q9QX99: Q9QX9A: Q9QX9B: Q9QX9C: Q9QX9D:
AC Q9QX9E: Q9QX9F;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Plectin 1 (PUN) (PCN) (Fragment).
GN PLEC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 111
SEQUENCE FROM N.A.; ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
AC TISSUE-Brain, Embryo, Heart, Kidney, Skeletal muscle, and Testis,
RX MEDLINE-20025755; PubMed-19556294;
RA Fuchs P., Zorner M., Reznicek G.A., Spazierer D., Gehler S.,
CA Gustafson M.J., Hauptmann R., Wiche G.;
F1 "Unusual 5' transcript complexity of plectin isoforms: novel tissue-
F1 specific exons modulate actin binding activity.";
F1 Hum. Mol. Genet. 8:2461-2472(1999).
RN 121
SEQUENCE OF 181-812 FROM N.A.
AC SPACTIN c44d.61; Tissue: Embryo.
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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RA Arakawa I., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamaki I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito K.,
RA Kadra K., Matsuda H.A., Ashburner M., Ratalecy S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King R., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki K., Tomita M., Wagner L., Washio I.,
RA Sakai K., Okido T., Furuno M., Aono H., Haidarceli R., Raish G.,
RA Blake J., Bollelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Holmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Marzocchi J., Mombertis P.,
RA Nordone P., Ring H., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Waga K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohisaki S.,
RA Hayashizaki Y.;
RA *Functional annotation of a full-length mouse cDNA collection.*;
RI Nature 409:685-690(2001).
CC -1- FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTUBULES AND
CC MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSESOMES OR
CC HEMIDESMOSESOMES. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND
CC STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT
CC ALSO IN THE REGULATION OF THEIR DYNAMICS.
CC -1- SURUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 16 ISOFORMS; PLEC-1, 2A (SHOWN HERE), PLEC-1,
CC PLEC-1A, PLEC-1B, 2A, PLEC-1B, PLEC-0, 1C, PLEC-0, 1C, 2A, PLEC-
CC 0, 1C, 2A, 3A, PLEC-1D, 2A, PLEC-1D, PLEC-1E, 2A, PLEC-1E, PLEC-1F,
CC PLEC-1G, PLEC-1H AND PLEC-1I; ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LUNG, BRAIN, SMALL
CC INTESTINE, MUSCLE, HEART AND SKIN WITH LOWER LEVELS FOUND IN
CC KIDNEY, LIVER, UTERUS, SPLEEN AND SALIVARY GLAND.
CC -1- DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH
CC VIMENTIN, DESMIN, GAP, CYTOKERATINS, LAMIN B, WHEREAS BOTH THE N-
CC AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
CC -1- PTM: PHOSPHORYLATED BY CMG2; REGULATES DISSOCIATION FROM
CC INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 SPECTRIN REPEATS.
CC -1- SIMILARITY: BELONGS TO THE PLEKIN OR CYTOLINKER FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
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CC EMBL: AF188006; AAF18066.1;
CC EMBL: AF188007; AAF18067.1;
CC EMBL: AF188008; AAF18068.1;
CC EMBL: AF188009; AAF18069.1;
CC EMBL: AF188010; AAF18070.1;
CC EMBL: AF188011; AAF18071.1;
CC EMBL: AF188012; AAF18072.1;
CC EMBL: AF188013; AAF18073.1;
CC EMBL: AF188014; AAF18074.1;
CC EMBL: AF188015; AAF18075.1;
CC EMBL: AF188016; AAF18076.1;
CC EMBL: AF188017; AAF18077.1;
CC EMBL: AF188018; AAF18078.1;
CC EMBL: AF188019; AAF18079.1;
CC EMBL: AF188020; AAF18080.1;
CC EMBL: AF188021; AAF18081.1;
CC EMBL: AF188022; AAF18082.1;
CC EMBL: AF188023; AAF18083.1;
CC EMBL: AK017743; BAR40907.1; ALT_INIT.
CC M3P. MG1.1-77961; Plect.
CC InterPro: IPR001589; Actbind_actnin.
CC InterPro: IPR001715; Calponin-like.

```


FT DOMAIN 1 192 ACTIN-BINDING.
 FT CH 1.
 FT CH 2.
 FT SPECTRIN 1.
 FT SPECTRIN 2.
 FT SPECTRIN 3.
 FT SPECTRIN 4.
 FT COILED COIL (POTENTIAL).
 FT PLECTIN 1.
 FT PLECTIN 2.
 FT PLECTIN 3.
 FT PLECTIN 4.
 FT PLECTIN 5.
 FT PLECTIN 6.
 FT PLECTIN 7.
 FT PLECTIN 8.
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 FT PLECTIN 24.
 FT PLECTIN 25.
 FT PLECTIN 26.
 FT PLECTIN 27.
 FT PLECTIN 28.
 FT PLECTIN 29.
 FT PLECTIN 30.
 FT PLECTIN 31.
 FT PLECTIN 32.
 FT BINDING TO INTERMEDIATE FILAMENTS (BY
 SIMILARITY).
 FT DOMAIN 4414 4429 4 X 4 AA LAMIN REPEATS OF C-S-R-X.
 FT MOD RES 4428 4438 PHOSPHORYLATION (BY CDC2).
 FT SEQUENCE 4473 AA: 509015 MW: 514461SD361E3484 CRC64;
 Query Match 63.6%; Score 35; DB 1; Length 4473.
 Best local similarity 63.6%; Prod. No. 3.6e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ELMRLQVKEE 11
 LB 205 ELGLRQVRE 215
 RESULT 13
 PLE1_HUMAN
 ID PLE1_HUMAN STANDARD; PRI: 4684 AA.
 AC Q15149; Q16640; Q15148;
 DI 16-06-2001 (Ref. 40, last sequence update)
 DI 16-06-2001 (Ref. 40, last sequence update)
 DI 16-06-2001 (Ref. 40, last annotation update)
 DE Plectin 1 (PLIN) (P'N) (Hemidesmosomal protein 1) (HDL).
 GN PLECL.
 OS Homo sapiens (human).
 OR Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OR Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OR NCBI TaxId 9606;
 RN [1]
 RC SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE: Placenta;
 RX MEDLINE 96210632; PubMed 8634055;
 RA Liu C.-G., Macrecker G., Gastanon M.J., Hauptmann R., Wiche G.;

RI "Human plectin: organization of the gene, sequence analysis, and
 chromosome localization (8924).";
 RL Euc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3). AND DISEASE.
 RX MEDLINE 96312447; PubMed 8698233;
 RA McLean W.H.I., Pulkkinen L., Smith F.J.D., Rugg E.L., Lane E.H.,
 Rullrich F., Burgeson R.P., Amano S., Hudson D.L., Owartha K.,
 McGrath J.A., McMillan J.R., Eady R.A.J., Leigh I.M., Christiano A.M.,
 Uitto J.;
 RA "Loss of plectin causes epidermolysis bullosa with muscular dystrophy:
 cDNA cloning and genomic organization.";
 RL Genes Dev. 10:1724-1735(1996).
 RN [3]
 RP VARIANT MD-EBS 1003-GLN-ALA-1005 DEL.
 RX MEDLINE 97049959; PubMed 8894687;
 RA Pulkkinen L., Smith F.J.D., Shimizu H., Murata S., Yacita H.,
 Hachisuka H., Nishikawa T., Melican W.H.I., Uitto J.;
 RA "Homozygous deletion mutations in the plectin gene (PLEC1) in patients
 with epidermolysis bullosa simplex associated with late-onset
 muscular dystrophy.";
 RL Hum. Mol. Genet. 5:1539-1545(1996).
 RN [4]
 RP VARIANT MD-EBS LEU-429 INS.
 RX MEDLINE 21090821; PubMed 11159198;
 RA Bauer J.W., Roudot F., Koflet B., Reznicek G.A., Kornacker L.,
 Muss W., Hamelner R., Klausberger A., Buber A., Pohl-Gubo G.,
 Wiche G., Uitto J., Hintner H.;
 RA "A compound heterozygous cys amino-acid insertion/deletion mutation in
 the plectin gene causes epidermolysis bullosa simplex with plectin
 deficiency.";
 RL Am. J. Pathol. 158:617-625(2001).
 CC -!- FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROFILAMENTS AND
 MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSESOMES OR
 HEMIDESMOSESOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO
 MEMBRANE COMPLEXES IN MUSCLE. MAY BE INVOLVED NOT ONLY IN THE
 CROSSLINKING AND STABILIZATION OF CYTOSKELETAL INTERMEDIATE
 FILAMENTS NETWORK, BUT ALSO IN THE REGULATION OF THEIR DYNAMICS.
 CC -!- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2 AND 3; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN
 MUSCLE, HEART, PLACENTA AND SPINAL CORD.
 CC -!- DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH
 VIMENTIN, DESMIN, GAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-
 AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
 CC -!- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM
 INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
 CC -!- DISEASE: DEFECTS IN PLECL ARE THE CAUSE OF EPIDERMOLYSIS BULLOSA
 WITH MUSCULAR DYSTROPHY (MD-EBS OR EB-MD), AN AUTOSOMAL RECESSIVE
 DISORDER CHARACTERIZED BY EPIDERMAL BLISTER FORMATION AT THE LEVEL
 OF THE HEMIDESMOSE AND ASSOCIATED LATE-ONSET MUSCULAR DYSTROPHY.
 CC -!- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
 CC -!- SIMILARITY: CONTAINS 33 PLECLIN REPEATS.
 CC -!- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
 CC -!- SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC EMBL: 254367; CAA91196.1;
 CC EMBL: U51204; AAB05427.1;
 CC EMBL: D63610; AAB05428.1;
 CC EMBL: D63609; AAB05428.1; JOINED.
 CC EMBL: X97053; CAA65765.1;
 CC HSP: Q01082; IHRK.
 CC Genew: HGNC:9069; PLECL.

TISSUE: Glial tumor;
 MEDLINE: 96210642; PubMed: 8644055;
 Liu C.-G., Maetcker C., Castanon M.J., Hauptmann R., Wiehe G.,
 "Human plectrin: organization of the gene, sequence analysis, and
 chromosome localization (4q24).",
 Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
 [4]
 PARTIAL SEQUENCE FROM N A (ISOFORMS 2: 3; 4), AND TISSUE SPECIFICITY
 TISSUE: Glial tumor;
 MEDLINE: 97421050; PubMed: 9177781;
 Elliott C.E., Becker B., Ochler S., Castanon M.J., Hauptmann R.,
 Wiehe G.,
 "Plectrin transcript diversity: identification and tissue distribution
 of variants with distinct first coding exons and rodless isoforms.",
 Genomics 42:115-125(1997).
 -1- FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROFILAMENTS AND
 HEMIDESMOSOMES. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND
 STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT
 ALSO IN THE REGULATION OF THEIR DYNAMICS.
 -1- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
 -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: 1 (SHOWN HERE), 2, 3 AND 4; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
 SKELETAL MUSCLE AND LOWEST IN THYMUS.
 -1- DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH
 VIMENTIN, DESMIN, GFAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-
 AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
 -1- PTM: PHOSPHORYLATED BY CK2; REGULATES DISSOCIATION FROM
 INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
 -1- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
 -1- SIMILARITY: CONTAINS 2 CALPAIN-HOMOLOG (CH) DOMAINS.
 -1- SIMILARITY: CONTAINS 3 PLECTIN REPEATS.
 -1- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
 -1- SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
 -1- CAUTION: ISOFORM 4 IS A FRAGMENT AT THE N-TERMINUS.

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 entities requires a license agreement (see <http://www.isb-sib.ch/actinome7>
 or send an email to license@isb-sib.ch).

 EMBL: X59601; CAA42169.1; ?
 EMBL: U96274; AAC53209.1; ?
 EMBL: U96275; AAC53210.1; ?
 EMBL: U96276; AAC53211.1; ?
 PIR: A39648; A39648.
 PIR: S21876; S21876.
 RSD: U01082; IHRK.
 InterPro: IPR001589; Actbind actin.
 InterPro: IPR001715; Calpainin-like.
 InterPro: IPR001101; plectin_repeat.
 InterPro: IPR005326; S10_pectrin.
 InterPro: IPR002017; Spectrin.
 Pfam: PF00407; Ch; 2.
 Pfam: PF00681; Plectin; 21.
 Pfam: PF03501; S10_pectrin; 1.
 SMART: SM00043; CH; 2.
 SMART: SM00250; PLEC; 3.
 SMART: SM00150; SPECT; 4.
 PROSITE: PS00019; ACTININ_1; FALSE_NBT.
 PROSITE: PS00020; ACTININ_2; FALSE_NBT.
 PROSITE: PS00021; CH; 2.
 Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding;
 Phosphorylation; Alternative splicing.
 Domain 1 1473 GLOBULAR 1.
 Domain 1474 2758 GLOBULAR 1.
 Domain 2759 4687 GLOBULAR 2.
 Domain 181 405 ACTIN-BINDING.
 Domain 185 288 CH 1.

FT	DOMAIN	301	403	CH 2.
FT	REPEAT	648	722	SPECTRIN 1.
FT	REPEAT	743	827	SPECTRIN 2.
FT	REPEAT	840	933	SPECTRIN 3.
FT	REPEAT	1318	1418	SPECTRIN 4.
FT	DOMAIN	1472	1692	COILED COIL (POTENTIAL).
FT	DOMAIN	1724	1760	COILED COIL (POTENTIAL).
FT	REPEAT	2791	2828	PLECTIN 1.
FT	REPEAT	2829	2866	PLECTIN 2.
FT	REPEAT	2867	2904	PLECTIN 3.
FT	REPEAT	2943	2980	PLECTIN 4.
FT	REPEAT	2984	3018	PLECTIN 5.
FT	REPEAT	3119	3156	PLECTIN 6.
FT	REPEAT	3157	3194	PLECTIN 7.
FT	REPEAT	3195	3232	PLECTIN 8.
FT	REPEAT	3233	3270	PLECTIN 9.
FT	REPEAT	3271	3308	PLECTIN 10.
FT	REPEAT	3311	3346	PLECTIN 11.
FT	REPEAT	3488	3525	PLECTIN 12.
FT	REPEAT	3526	3563	PLECTIN 13.
FT	REPEAT	3564	3601	PLECTIN 14.
FT	REPEAT	3602	3639	PLECTIN 15.
FT	REPEAT	3643	3677	PLECTIN 16.
FT	REPEAT	3823	3860	PLECTIN 17.
FT	REPEAT	3861	3898	PLECTIN 18.
FT	REPEAT	3899	3936	PLECTIN 19.
FT	REPEAT	3937	3974	PLECTIN 20.
FT	REPEAT	3978	4011	PLECTIN 21.
FT	REPEAT	4066	4103	PLECTIN 22.
FT	REPEAT	4104	4141	PLECTIN 23.
FT	REPEAT	4142	4179	PLECTIN 24.
FT	REPEAT	4180	4217	PLECTIN 25.
FT	REPEAT	4221	4255	PLECTIN 26.
FT	REPEAT	4256	4308	PLECTIN 27.
FT	REPEAT	4411	4448	PLECTIN 28.
FT	REPEAT	4449	4486	PLECTIN 29.
FT	REPEAT	4487	4524	PLECTIN 30.
FT	REPEAT	4525	4562	PLECTIN 31.
FT	REPEAT	4563	4600	PLECTIN 32.
FT	REPEAT	4628	4643	PLECTIN 33.
FT	DOMAIN	4628	4643	4 X 4 AA TANDEM REPEATS OF G-S-R-X.
FT	M-RES	4542	4542	PHOSPHORYLATION (BY CDC2) (BY SIMILARITY).
FT	VARSPLIC	1	180	MYOIMPLDQRLAIYEVILFRGVNVAKKRRPRSLHHVP
FT				GVNIOVMKAMTSLKARGIVRRTFAWCHFYWYLLNEGIDHL
FT				ROYLHLPPEIVIASIQVRVRPVAVMVARRKSPHVQMOGP
FT				LGCPKRGPLPAEDPAPEEPQVYRKEEGAPETPVVSAT
FT				IVGTILARGCPPTPAT -> MSQQLRYDEPEGLSKRTSS
FT				EDNLYLAVLRASEGKK (IN ISOFORM 2).
FT	VARSPLIC	1	180	MYOIMPLDQRLAIYEVILFRGVNVAKKRRPRSLHHVP
FT				GVNIOVMKAMTSLKARGIVRRTFAWCHFYWYLLNEGIDHL
FT				ROYLHLPPEIVIASIQVRVRPVAVMVARRKSPHVQMOGP
FT				LGCPKRGPLPAEDPAPEEPQVYRKEEGAPETPVVSAT
FT				IVGTILARGCPPTPAT -> MEPSGLFSLVWVGHVVSLSA
FT				AVHWKRGHROADEU (IN ISOFORM 3).
FT	VARSPLIC	1	180	MYOIMPLDQRLAIYEVILFRGVNVAKKRRPRSLHHVP
FT				GVNIOVMKAMTSLKARGIVRRTFAWCHFYWYLLNEGIDHL
FT				ROYLHLPPEIVIASIQVRVRPVAVMVARRKSPHVQMOGP
FT				LGCPKRGPLPAEDPAPEEPQVYRKEEGAPETPVVSAT
FT				IVGTILARGCPPTPAT -> IVSNSSGSSPSGDTLPWNLG
FT				KTORSRGGSGSVGNGSVLDPAERAVIRIA (IN ISOFORM 4)
SO	SEQUENCE	4687 AA;	533527 MW;	9966CAP71H929751 CR664;

Query Match: Score 35; DB 1; Length 4687;
 Best Local Similarity: 63.6%; Pred. No. 3.8e+02;
 Matches: 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ELMRLQDDEE 11
 Db 419 ELQIRWQDEYE 429

